

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/785,607A  
Source: IFW/b  
Date Processed by STIC: 7/15/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/785/607A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line **not** exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
  
- 5      Variable Length     Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)          missing. If intentional, please insert the following lines for **each** skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)          missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10     Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11     Use of <220>     Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12     PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13     Misuse of n/Xaa     "**n**" can only represent a single nucleotide; "**Xaa**" can only represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 07/15/2005

PATENT APPLICATION: US/10/785,607A

TIME: 11:09:25

Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT

Output Set: N:\CRF4\07152005\J785607A.raw

4 <110> APPLICANT: Ashkenazi, Avi J.  
 5 Fong, Sherman  
 6 Goddard, Audrey  
 7 Gurney, Austin L.  
 8 Napier, Mary A.  
 9 Tumas, Daniel  
 10 Wood, William I.  
 12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR  
 13 THE TREATMENT OF DISEASES CHARACTERIZED BY A-33 RELATED  
 14 ANTIGENS  
 16 <130> FILE REFERENCE: 39780-1216R1C1D5  
 18 <140> CURRENT APPLICATION NUMBER: US 10/785,607A  
 19 <141> CURRENT FILING DATE: 2004-02-24  
 21 <150> PRIOR APPLICATION NUMBER: US 09/953,499  
 22 <151> PRIOR FILING DATE: 2001-09-14  
 24 <150> PRIOR APPLICATION NUMBER: US 09/254,465  
 25 <151> PRIOR FILING DATE: 1999-03-05  
 27 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855  
 28 <151> PRIOR FILING DATE: 1998-11-20  
 30 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437  
 31 <151> PRIOR FILING DATE: 1998-09-17  
 33 <160> NUMBER OF SEQ ID NOS: 30  
 35 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 37 <210> SEQ ID NO: 1  
 38 <211> LENGTH: 299  
 39 <212> TYPE: PRT  
 40 <213> ORGANISM: Homo sapiens  
 42 <400> SEQUENCE: 1  
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 45 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 46 20 25 30  
 47 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 48 35 40 45  
 49 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 50 55 60  
 51 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 52 65 70 75 80  
 53 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 54 85 90 95  
 55 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 56 100 105 110  
 57 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val

Does Not Comply  
Corrected Diskette Needed

pp 3-4

## RAW SEQUENCE LISTING

DATE: 07/15/2005

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Output Set: N:\CRF4\07152005\J785607A.raw

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61 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
62 145          150          155          160
63 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
64          165          170          175
65 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
66          180          185          190
67 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
68          195          200          205
69 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
70          210          215          220
71 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
72 225          230          235          240
73 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
74          245          250          255
75 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
76          260          265          270
77 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
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80          290          295
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85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
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92          20          25          30
93 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
94          35          40          45
95 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
96          50          55          60
97 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
98 65          70          75          80
99 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
100          85          90          95
101 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
102          100          105          110
103 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
104          115          120          125
105 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
106          130          135          140
107 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
108 145          150          155          160
109 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile

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Output Set: N:\CRF4\07152005\J785607A.raw

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112              180              185              190
113 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
114              195              200              205
115 Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
116              210              215              220
117 Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
118 225              230              235              240
119 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
120              245              250              255
121 Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
122              260              265              270
123 Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
124              275              280              285
125 Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
126              290              295              300
127 Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His Val Tyr Glu Ala Ala
128 305              310              315              320
129 Arg
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134 <211> LENGTH: 390
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Artificial sequence
141 <400> SEQUENCE: 3
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143 ttgtatggtc tctgaggaag gcggaacag ctatggggag gtcaagggtca agctcatcgt 120
144 gcttgtgcct ccatacaagc ctacagttaa catccctcc tctgccacca ttgggaaccg 180
145 ggcagtgtcg acatgctcag aacaagatgg ttccccacct tctgaataca cctggttcaa 240
146 agatgggata gtgatgccta cgaatcccaa aagcaccctg gccttcagca actcttcta 300
147 tgtcttgaat cccacaacag gagagctggt ctttgatccc ctgtcagcct ctgatactgg 360
148 agaatacagc tgtgaggcac ggaatgggta
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151 <211> LENGTH: 726
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Artificial sequence
158 <400> SEQUENCE: 4
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161 tgttgtgcct cttcatattg gcgatcctgt tgtgtccct ggcattgggc agtggttacag 180
162 ttgcactctt ctgaacctga agtcagaatt cctgagaata atcctgtgaa gttgtcctgt 240
163 gcctactcgg gcttttcttc tccccgtgtg gagtgggaag ttgaccaagg agacaccacc 300
164 agactcgttt gctataataa caagatcaca gcttcctatg aggaccgggt gaccttcttg 360
165 ccaactggta tcaccttcaa gtccgtgaca cgggaagaca ctgggacata cacttgatatg 420
166 gtctctgagg aaggcggcaa cagctatggg gagggtcaagg tcaagctcat cgtgcttggtg 480

```

*insufficient exploration - give source of genetic material (see item 11 on Enva summary sheet)*

*same env*

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Output Set: N:\CRF4\07152005\J785607A.raw

167 cctccatcca agcctacagt taacatcccc tcctctgcca ccattgggaa ccgggcagtg 540  
 168 ctgacatgct cagaacaaga tgggtcccca ccttctgaat acacctggtt caaagatggg 600  
 169 atagtgatgc ctacgaatcc caaaagcacc cgtgccttca gcaactcttc ctatgtcctg 660  
 170 aatcccacaa caggagagct ggtctttgat cccctgtcag cctctgatac tggagaatac 720  
 171 agctgt 726

173 &lt;210&gt; SEQ ID NO: 5

174 &lt;211&gt; LENGTH: 1503

175 &lt;212&gt; TYPE: DNA

176 &lt;213&gt; ORGANISM: Artificial Sequence

178 &lt;220&gt; FEATURE:

179 &lt;223&gt; OTHER INFORMATION: Artificial sequence

181 &lt;400&gt; SEQUENCE: 5

182 gcaggcaaag taccagggcc gcctgcatgt gagccacaag gttccaggag atgtatccct 60  
 183 ccaattgagc accctggaga tggatgaccg gagccactac acgtgtgaag tcacctggca 120  
 184 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180  
 185 ctctgtctcc aagcccacag tgacaactgg cagcgggttat ggcttcacgg tggcccaggg 240  
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 189 ggctctgagc agcacagcga cattgtgaag tttgtggtca aagactctc aaagctactc 480  
 190 aagaccaaga ctgaggcacc tacaacctatg acataccctc tgaaagcaac atctacagt 540  
 191 aagcagtcct gggactggac cactgacatg gatggctacc ttggagagac cagtgtctgg 600  
 192 ccaggaaaga gcctgcctgt ctttgccatc atcctcatca tctccttggt ctgtatgggt 660  
 193 gtttttacca tggcctatat catgctctgt cggaagacat cccaacaaga gcatgtctac 720  
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 197 cgcccgctg ctggacacag ttcctctgga ttatgagttt ctggccactg agggcaaaag 960  
 198 tgtctgttaa aaatgcccc ttaggccagg atctgctgac ataattgcct agtcagtcct 1020  
 199 tgcttctgc atggccttct tccctgtac ctctcttct ggatagcca agtgtccgc 1080  
 200 ctaccaacac tggagccgct gggagtcact ggctttgccc tggaaattgc cagatgcac 1140  
 201 tcaagtaagc cagctgctgg atttgctct gggccctct agtatctct cggggggtt 1200  
 202 ctgggtactcc tctctaaata ccagagggaa gatgcccata gcactaggac ttgggtcatc 1260  
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 205 cagcttttaa ttgaaattgt tatttcacag gccagggttc agttctgctc ctccactata 1440  
 206 agtctaattgt tctgactctc tcctggtgct caataaatat ctaatcataa cagcaaaaaa 1500  
 207 aaa 1503

209 &lt;210&gt; SEQ ID NO: 6

210 &lt;211&gt; LENGTH: 319

211 &lt;212&gt; TYPE: PRT

212 &lt;213&gt; ORGANISM: Homo sapiens

214 &lt;400&gt; SEQUENCE: 6

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 216 1 5 10 15  
 217 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg  
 218 20 25 30  
 219 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser  
 220 35 40 45

*This error appears in  
 subsequent sequences, too.*

## RAW SEQUENCE LISTING

DATE: 07/15/2005

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TIME: 11:09:25

Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT

Output Set: N:\CRF4\07152005\J785607A.raw

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221 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
222      50                      55                      60
223 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
224 65                      70                      75                      80
225 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
226                      85                      90                      95
227 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
228                      100                     105                     110
229 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
230                      115                     120                     125
231 Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
232                      130                     135                     140
233 Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
234 145                      150                      155                      160
235 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
236                      165                      170                      175
237 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
238                      180                      185                      190
239 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
240                      195                      200                      205
241 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
242                      210                      215                      220
243 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
244 225                      230                      235                      240
245 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
246                      245                      250                      255
247 Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
248                      260                      265                      270
249 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
250                      275                      280                      285
251 Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
252                      290                      295                      300
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254 305                      310                      315
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259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
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265 ggggatctta ctgggcctgc tactcctggg gcaccttaaca gtggacactt atggccgtcc 180
266 catcctggaa gtgccagaga gtgtaacagg accttggaata ggggatgtga atcttccttg 240
267 cacctatgac cccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300
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270 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacctggc agactcctga 480
271 tggaaccaa gtcgtgagag ataagattac tgagctccgt gtccagaaac tctctgtctc 540
272 caagcccaca gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600

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VERIFICATION SUMMARY

DATE: 07/15/2005

PATENT APPLICATION: US/10/785,607A

TIME: 11:09:26

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